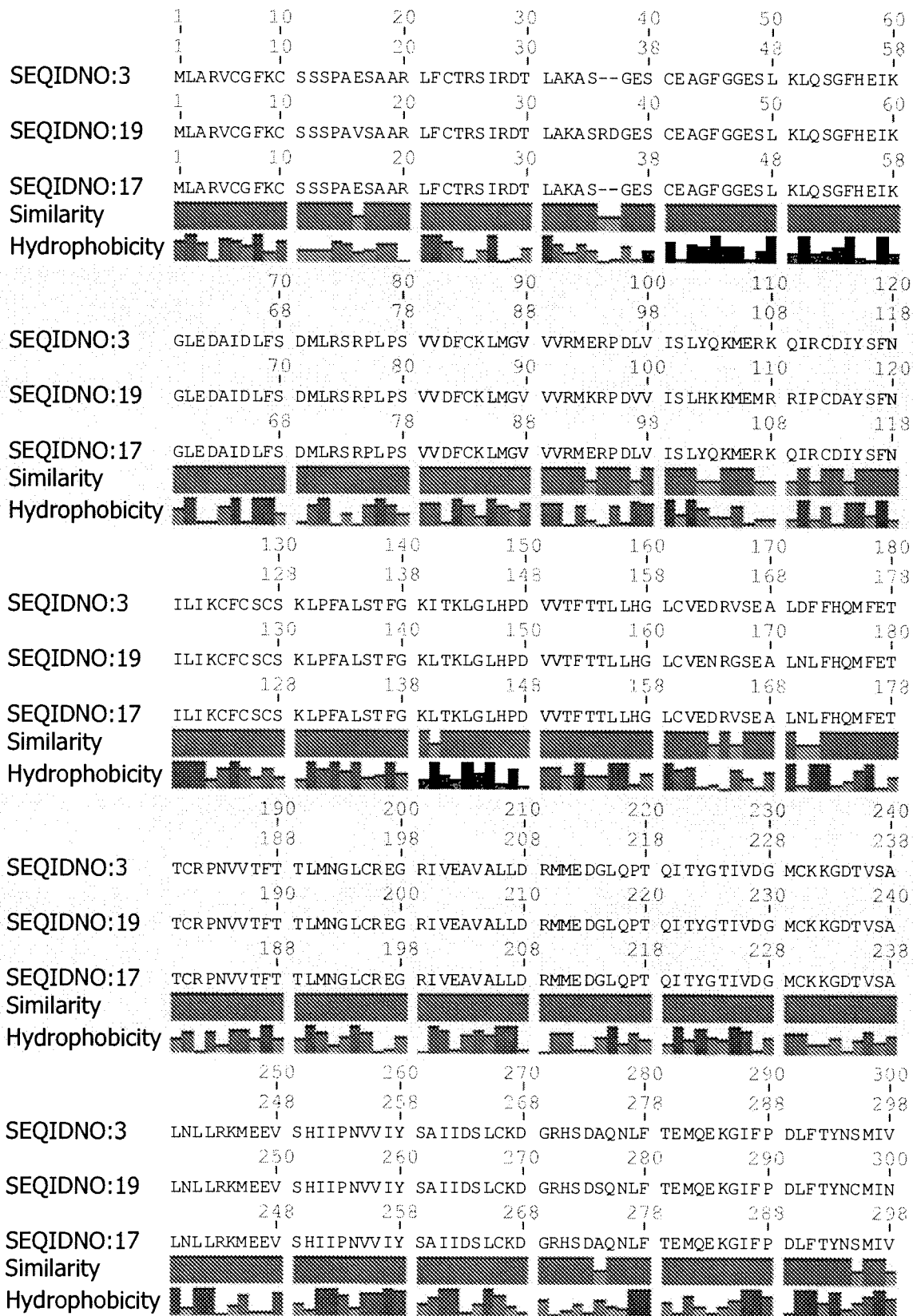
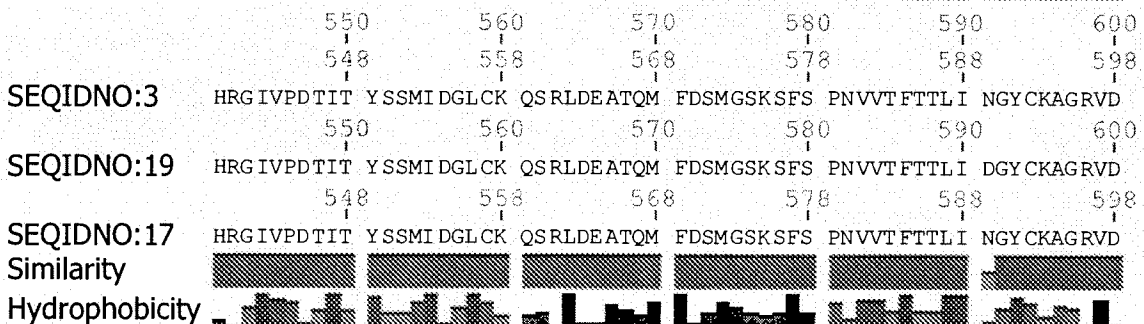
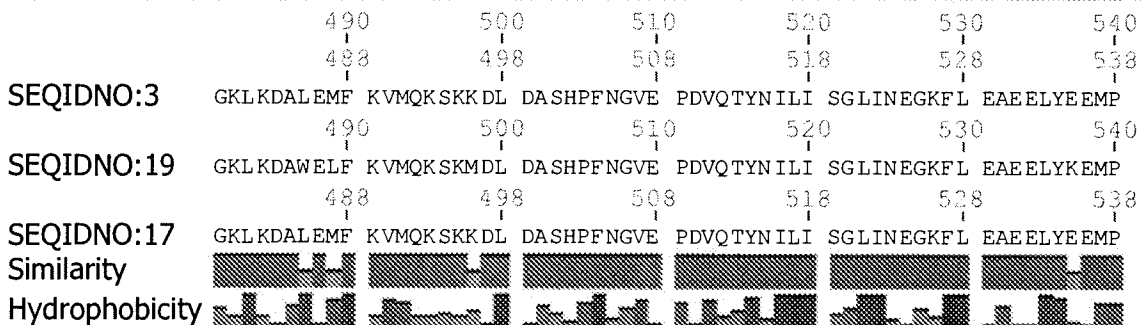
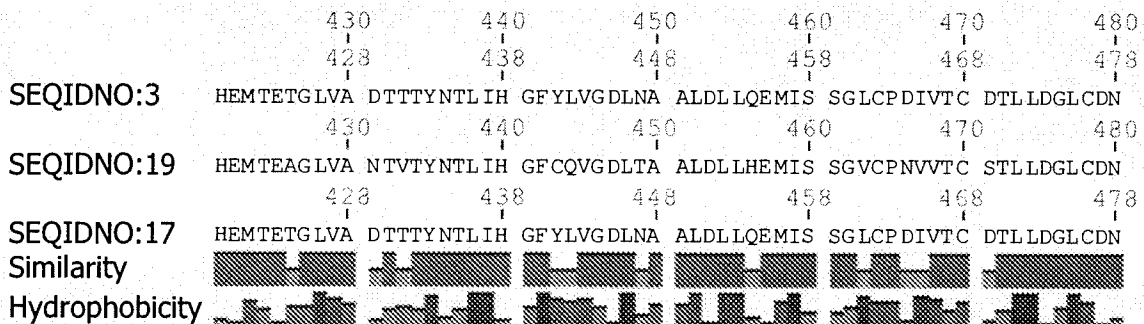
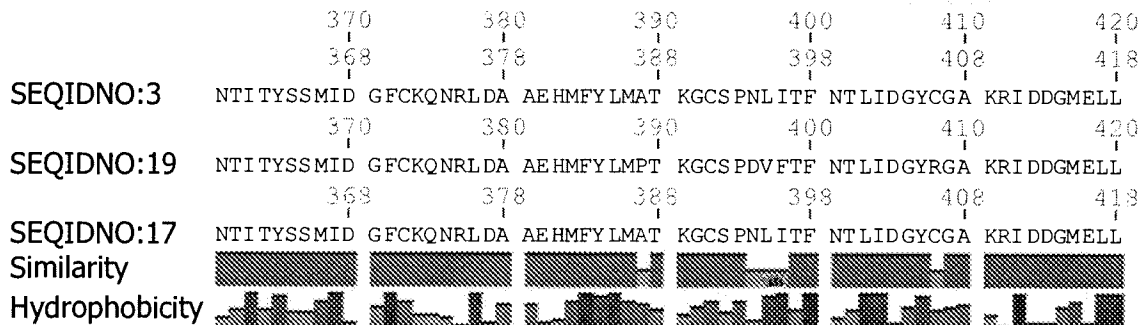
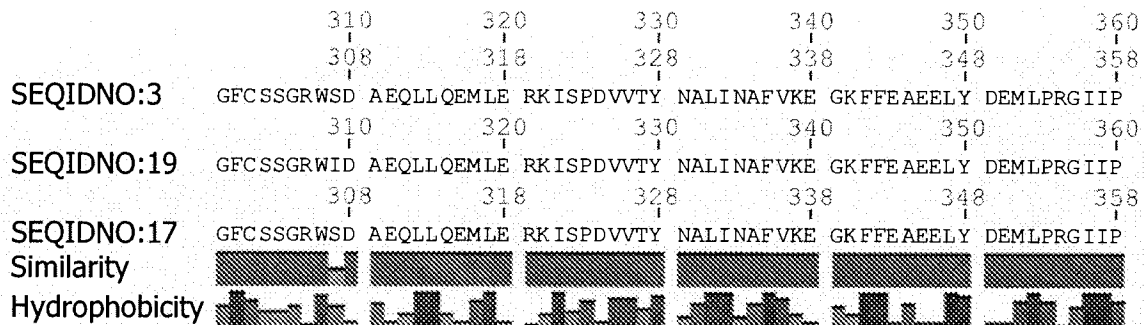
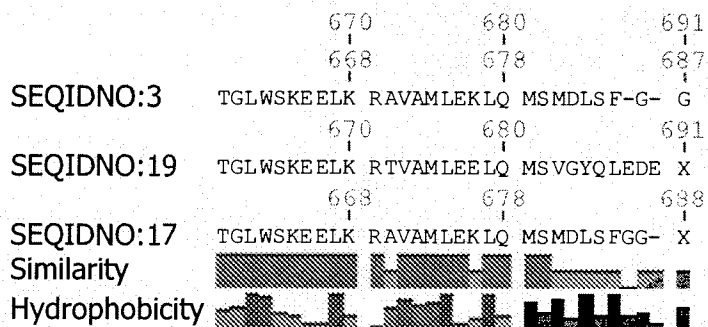
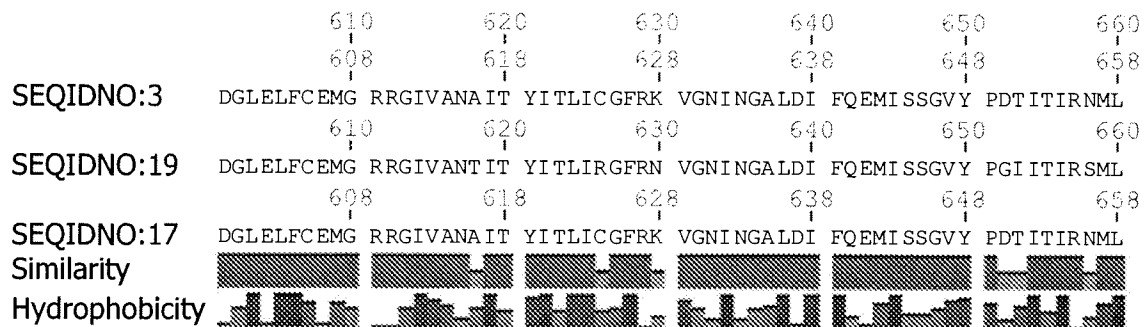


Application No.	: 10/613,053	Confirmation No.:	6718
Applicant:	: Imamura		
Filed:	: July 7, 2003		
Group Art Unit:	1638		
Examiner:	: FOX, David T.		
For	: Protein Involved in Restoration of Cytoplasmic Male Sterility to Fertility and Gene Encoding the Protein and Gene		
Docket No.	: 54-05A		
Customer No.	: 23713		

APPENDIX A and APPENDIX B







	1	10	20	30	40	50	60	70
seqidno2	1	10	20	30	40	50	60	70
	1	10	20	30	40	50	60	70
seqidno18	1	10	20	30	40	50	60	70
seqidno16	1	10	20	30	40	50	60	70
Similarity								
	80	90	100	110	120	130	140	
seqidno2	80	90	100	110	120	130	140	
seqidno18	80	90	100	110	120	130	140	
seqidno16	80	90	100	110	120	130	140	
Similarity								
	150	160	170	180	190	200	210	
seqidno2	150	160	170	180	190	200	210	
seqidno18	150	160	170	180	190	200	210	
seqidno16	150	160	170	180	190	200	210	
Similarity								
	220	230	240	250	260	270	280	
seqidno2	220	230	240	250	260	270	280	
seqidno18	220	230	240	250	260	270	280	
seqidno16	220	230	240	250	260	270	280	
Similarity								
	290	300	310	320	330	340	350	
seqidno2	290	300	310	320	330	340	350	
seqidno18	290	300	310	320	330	340	350	
seqidno16	290	300	310	320	330	340	350	
Similarity								

		360	370	380	390	400	410	420
		351	361	371	381	391	401	411
seqidno2	ATACAGCTTC	AATATTCTGA	TAAAATGTTT	CTGCAGCTGC	TCTAAGCTCC	CCTTTGCTTT	GTCTACATTT	
		357	367	377	387	397	407	417
seqidno18	ATACAGCTTC	AATATTCTGA	TAAAGTGTTT	CTGCAGCTGC	TCTAAGCTGC	CCTTTGCTTT	GTCTACATTT	
		351	361	371	381	391	401	411
seqidno16	ATACAGCTTC	AATATTCTGA	TAAAATGTTT	CTGCAGCTGC	TCTAAGCTCC	CCTTTGCTTT	GTCTACATTT	
Similarity								
		430	440	450	460	470	480	490
		421	431	441	451	461	471	481
seqidno2	GGTAAGATCA	CCAAGCTTGG	ACTCCACCCT	GATGTTGTTA	CCTTCACCAC	CCTGCTCCAT	GGATTATGTG	
		427	437	447	457	467	477	487
seqidno18	GGTAAGCTCA	CCAAGCTTGG	ACTCCACCCT	GATGTTGTTA	CCTTCACCAC	CCTTCTCCAC	GGATTGTGTG	
		421	431	441	451	461	471	481
seqidno16	GGTAAGCTCA	CCAAGCTTGG	ACTCCACCCT	GATGTTGTTA	CCTTCACCAC	CCTGCTCCAC	GGATTGTGCG	
Similarity								
		500	510	520	530	540	550	560
		491	501	511	521	531	541	551
seqidno2	TGGAAGATAG	GGTTTCTGAA	GCCTTGATT	TTTTTCATCA	AATGTTTGAA	ACGACATGTA	GGCCCAATGT	
		497	507	517	527	537	547	557
seqidno18	TGGAATAATAG	GGGTTCTGAA	GCTTTGAATT	TGTTTCATCA	AATGTTTGAA	ACGRCATGTA	GGCCCAATGT	
		491	501	511	521	531	541	551
seqidno16	TGGAAGATAG	GGTTTCTGAA	GCTTTGAATT	TGTTTCATCA	AATGTTTGAA	ACGACATGTA	GGCCCAATGT	
Similarity								
		570	580	590	600	610	620	630
		561	571	581	591	601	611	621
seqidno2	CGTAACCTTC	ACCACTTTGA	TGAACGGTCT	TTGCCGCGAG	GGTAGAATTG	TCGAAGCCGT	AGCTCTGCTT	
		567	577	587	597	607	617	627
seqidno18	CGTAACCTTC	ACCACTTTGA	TGAACGGTCT	TTGCCGCGAG	GGTAGAATTG	TCGAAGCCGT	AGCTCTACTT	
		561	571	581	591	601	611	621
seqidno16	CGTAACCTTC	ACCACTTTGA	TGAACGGTCT	TTGCCGCGAG	GGTAGAATTG	TCGAAGCCGT	AGCTCTGCTT	
Similarity								
		640	650	660	670	680	690	700
		631	641	651	661	671	681	691
seqidno2	GATCGGATGA	TGGAAGATGG	TCTCCAGCCT	ACCCAGATTA	CTTATGGAAC	AATCGTAGAT	GGGATGTGTA	
		637	647	657	667	677	687	697
seqidno18	GATCGGATGA	TGGAAGATGG	TCTCCAGCCT	ACCCAGATTA	CTTATGGAAC	AATCGTAGAT	GGGATGTGTA	
		631	641	651	661	671	681	691
seqidno16	GATCGGATGA	TGGAAGATGG	TCTCCAGCCT	ACCCAGATTA	CTTATGGAAC	AATCGTAGAT	GGGATGTGTA	
Similarity								

	710	720	730	740	750	760	770
	701	711	721	731	741	751	761
seqidno2	AGAAGGGAGA	TACTGTGTCT	GCACTGAATC	TGCTGAGGAA	GATGGAGGAG	GTGAGCCACA	TCATACCCAA
	707	717	727	737	747	757	767
seqidno18	AGAAGGGAGA	TACTGTGTCT	GCACTGAATC	TGCTGAGGAA	GATGGAGGAG	GTGAGCCACA	TCATACCCAA
	701	711	721	731	741	751	761
seqidno16	AGAAGGGAGA	TACTGTGTCT	GCACTGAATC	TGCTGAGGAA	GATGGAGGAG	GTGAGCCACA	TCATACCCAA
Similarity							
	780	790	800	810	820	830	840
	771	781	791	801	811	821	831
seqidno2	TGTTGTAATC	TATAGTGCAA	TCATTGATAG	CCTTTGTAAA	GACGGACGTC	ATAGCGATGC	ACAAAATCTT
	777	787	797	807	817	827	837
seqidno18	TGTTGTAATC	TATAGTGCAA	TCATTGATAG	CCTTTGTAAA	GACGGACGTC	ATAGCGATTC	TCAAAAATCTT
	771	781	791	801	811	821	831
seqidno16	TGTTGTAATC	TATAGTGCAA	TCATTGATAG	CCTTTGTAAA	GACGGACGTC	ATAGCGATGC	ACAAAATCTT
Similarity							
	850	860	870	880	890	900	910
	841	851	861	871	881	891	899
seqidno2	TTCACTGAAA	TGCAAGAGAA	AGGAATCTTT	CCCGATTAT	TTACCTACAA	CAGTATGAT-	-AGTTGGTTT
	847	857	867	877	887	897	905
seqidno18	TTCACTGAAA	TGCAAGAGAA	AGGAATCTTT	CCAGATTAT	TTACCTACAA	CTGTATGATC	AA--CGGGTT
	841	851	861	871	881	891	899
seqidno16	TTCACTGAAA	TGCAAGAGAA	AGGAATCTTT	CCCGATTAT	TTACCTACAA	CAGTATGAT-	-AGTTGGTTT
Similarity							
	920	930	940	950	960	970	980
	909	919	929	939	949	959	969
seqidno2	TTGTAGCTCT	GGTAGATGGA	GCGACGCGGA	GCAGTTGTTG	CAAGAAATGT	TAGAAAGGAA	GATCAGCCCT
	915	925	935	945	955	965	975
seqidno18	TTGTAGCTCT	GGTAGATGGA	TCGACGCGGA	GCAGTTGTTG	CAAGAAATGT	TAGAAAGGAA	GATCAGCCCT
	909	919	929	939	949	959	969
seqidno16	TTGTAGCTCT	GGTAGATGGA	GCGACGCGGA	GCAGTTGTTG	CAAGAAATGT	TAGAAAGGAA	GATCAGCCCT
Similarity							
	990	1,000	1,010	1,020	1,030	1,040	1,050
	979	989	999	1,009	1,019	1,029	1,039
seqidno2	GATGTTGTAA	CTTATAATGC	TTTGATCAAT	GCATTTGTCA	AGGAAGGCAA	GTTCTTTGAG	GCTGAAGAAT
	985	995	1,005	1,015	1,025	1,035	1,045
seqidno18	GATGTTGTAA	CTTATAATGC	TTTGATCAAT	GCATTTGTCA	AGGAAGGCAA	GTTCTTTGAG	GCTGAAGAAT
	979	989	999	1,009	1,019	1,029	1,039
seqidno16	GATGTTGTAA	CTTATAATGC	TTTGATCAAT	GCATTTGTCA	AGGAAGGCAA	GTTCTTTGAG	GCTGAAGAAT
Similarity							

		1,060	1,070	1,080	1,090	1,100	1,110	1,120
		1,049	1,059	1,069	1,079	1,089	1,099	1,109
seqidno2	TATACGATGA	GATGCTTCCA	AGGGGTATAA	TCCCTAATAC	AATCACATAT	AGTTCAATGA	TCGATGGATT	
		1,055	1,065	1,075	1,085	1,095	1,105	1,115
seqidno18	TATACGATGA	GATGCTTCCT	AGGGGTATAA	TCCCTAATAC	AATCACATAT	AGTTCAATGA	TCGATGGATT	
		1,049	1,059	1,069	1,079	1,089	1,099	1,109
seqidno16	TATACGATGA	GATGCTTCCA	AGGGGTATAA	TCCCTAATAC	AATCACATAT	AGTTCAATGA	TCGATGGATT	
Similarity								
		1,130	1,140	1,150	1,160	1,170	1,180	1,190
		1,119	1,129	1,139	1,149	1,159	1,169	1,179
seqidno2	TTGCAAACAG	AATCGTCTTG	ATGCTGCTGA	GCACATGTTT	TATTTGATGG	CTACCAAGGG	CTGCTCTCCC	
		1,125	1,135	1,145	1,155	1,165	1,175	1,185
seqidno18	TTGCAAACAG	AATCGTCTTG	ATGCTGCTGA	GCACATGTTT	TATTTGATGC	CTACCAAGGG	CTGCTCTCCG	
		1,119	1,129	1,139	1,149	1,159	1,169	1,179
seqidno16	TTGCAAACAG	AATCGTCTTG	ATGCTGCTGA	GCACATGTTT	TATTTGATGG	CTACCAAGGG	CTGCTCTCCC	
Similarity								
		1,200	1,210	1,220	1,230	1,240	1,250	1,260
		1,189	1,199	1,209	1,219	1,229	1,239	1,249
seqidno2	AACCTAATCA	CTTTCAATAC	TCTCATAGAC	GGATATTGTG	GGGCTAAGAG	GATAGATGAT	GGAATGGAAC	
		1,195	1,205	1,215	1,225	1,235	1,245	1,255
seqidno18	GACGTATTCA	CTTTCAATAC	TCTCATAGAC	GGATATCGTG	GGGCTAAGAG	GATAGATGAT	GGAATGGAAC	
		1,189	1,199	1,209	1,219	1,229	1,239	1,249
seqidno16	AACCTAATCA	CTTTCAATAC	TCTCATAGAC	GGATATTGTG	GGGCTAAGAG	GATAGATGAT	GGAATGGAAC	
Similarity								
		1,270	1,280	1,290	1,300	1,310	1,320	1,330
		1,259	1,269	1,279	1,289	1,299	1,309	1,319
seqidno2	TTCTCCATGA	GATGACTGAA	ACAGGATTAG	TTGCTGACAC	AACTACTTAC	AACACTCTTA	TTCACGGGTT	
		1,265	1,275	1,285	1,295	1,305	1,315	1,325
seqidno18	TTCTCCATGA	GATGACTGAA	GCAGGATTAG	TTGCTAACAC	AGTTACTTAC	AACACTCTTA	TTCACGGGTT	
		1,259	1,269	1,279	1,289	1,299	1,309	1,319
seqidno16	TTCTCCATGA	GATGACTGAA	ACAGGATTAG	TTGCTGACAC	AACTACTTAC	AACACTCTTA	TTCACGGGTT	
Similarity								
		1,340	1,350	1,360	1,370	1,380	1,390	1,400
		1,329	1,339	1,349	1,359	1,369	1,379	1,389
seqidno2	CTATCTGGTG	GGCGATCTTA	ATGCTGCTCT	AGACCTTTTA	CAAGAGATGA	TCTCTAGTGG	TTTGTGCCCT	
		1,335	1,345	1,355	1,365	1,375	1,385	1,395
seqidno18	TTGTCAGGTG	GGCGATCTTA	CTGCTGCTCT	AGACCTTCTA	CATGAGATGA	TTTCTAGTGG	TGTGTGCCCT	
		1,329	1,339	1,349	1,359	1,369	1,379	1,389
seqidno16	CTATCTGGTG	GGCGATCTTA	ATGCTGCTCT	AGACCTTTTA	CAAGAGATGA	TCTCTAGTGG	TTTGTGCCCT	
Similarity								

	1,410	1,420	1,430	1,440	1,450	1,460	1,470
	1,399	1,409	1,419	1,429	1,439	1,449	1,459
seqidno2	GATATCGTTA	CTTGTGACAC	TTTGCTGGAT	GGTCTCTGCG	ATAATGGGAA	ACTAAAAGAT	GCATTGGAAA
	1,405	1,415	1,425	1,435	1,445	1,455	1,465
seqidno18	AATGTCGTTA	CTTGTAGCAC	TTTGCTGGAT	GGTCTCTGCG	ATAACGGGAA	ACTAAAAGAT	GCATGGGAAC
	1,399	1,409	1,419	1,429	1,439	1,449	1,459
seqidno16	GATATCGTTA	CTTGTGACAC	TTTGCTGGAT	GGTCTCTGCG	ATAATGGGAA	ACTAAAAGAT	GCATTGGAAA
Similarity							
	1,480	1,490	1,500	1,510	1,520	1,530	1,540
	1,469	1,479	1,489	1,499	1,509	1,519	1,529
seqidno2	TGTTTAAGGT	TATGCAGAAG	AGTAAGAAGG	ATCTTGATGC	TAGTCACCCC	TTCAATGGTG	TGGAACCTGA
	1,475	1,485	1,495	1,505	1,515	1,525	1,535
seqidno18	TGTTTAAGGT	TATGCAGAAG	AGTAAGATGG	ATCTTGATGC	TAGTCACCCC	TTCAATGGTG	TGGAACCTGA
	1,469	1,479	1,489	1,499	1,509	1,519	1,529
seqidno16	TGTTTAAGGT	TATGCAGAAG	AGTAAGAAGG	ATCTTGATGC	TAGTCACCCC	TTCAATGGTG	TGGAACCTGA
Similarity							
	1,550	1,560	1,570	1,580	1,590	1,600	1,610
	1,539	1,549	1,559	1,569	1,579	1,589	1,599
seqidno2	TGTTCAAAC	TACAAATATAT	TGATCAGCGG	CTTGATCAAT	GAAGGGAAGT	TTTATAGAGC	CGAGGAATTA
	1,545	1,555	1,565	1,575	1,585	1,595	1,605
seqidno18	TGTTCAAAC	TACAAATATAT	TGATCAGCGG	CTTGATCAAT	GAAGGGAAGT	TTTATAGAGC	TGAGGAATTA
	1,539	1,549	1,559	1,569	1,579	1,589	1,599
seqidno16	TGTTCAAAC	TACAAATATAT	TGATCAGCGG	CTTGATCAAT	GAAGGGAAGT	TTTATAGAGC	CGAGGAATTA
Similarity							
	1,620	1,630	1,640	1,650	1,660	1,670	1,680
	1,609	1,619	1,629	1,639	1,649	1,659	1,669
seqidno2	TACGAGGAGA	TGCCCCACAG	GGGTATAGTC	CCAGATACTA	TCACCTATAG	CTCAATGATC	GATGGATTAT
	1,615	1,625	1,635	1,645	1,655	1,665	1,675
seqidno18	TACAAGGAGA	TGCCCCACAG	GGGTATAGTC	CCAGATACTA	TTACCTATAG	CTCAATGATC	GATGGACTAT
	1,609	1,619	1,629	1,639	1,649	1,659	1,669
seqidno16	TACGAGGAGA	TGCCCCACAG	GGGTATAGTC	CCAGATACTA	TCACCTATAG	CTCAATGATC	GATGGATTAT
Similarity							
	1,690	1,700	1,710	1,720	1,730	1,740	1,750
	1,679	1,689	1,699	1,709	1,719	1,729	1,739
seqidno2	GCAAGCAGAG	CCGCCTAGAT	GAGGCTACAC	AAATGTTTGA	TTCGATGGGT	AGCAAGAGCT	TCTCTCCAAA
	1,685	1,695	1,705	1,715	1,725	1,735	1,745
seqidno18	GCAAGCAGAG	CCGCCTGGAT	GAGGCTACAC	AAATGTTTGA	TTCGATGGGT	AGCAAGAGCT	TCTCTCCAAA
	1,679	1,689	1,699	1,709	1,719	1,729	1,739
seqidno16	GCAAGCAGAG	CCGCCTAGAT	GAGGCTACAC	AAATGTTTGA	TTCGATGGGT	AGCAAGAGCT	TCTCTCCAAA
Similarity							

		1,760	1,770	1,780	1,790	1,800	1,810	1,820
		1,749	1,759	1,769	1,779	1,789	1,799	1,809
seqidno2	CGTAGTGACC	TTTACTACAC	TCATTAATGG	CTACTGTAAG	GCAGGAAGGG	TTGATGATGG	GCTGGAGCTT	
		1,755	1,765	1,775	1,785	1,795	1,805	1,815
seqidno18	CGTAGTGACC	TTTACTACAC	TCATTGATGG	CTACTGTAAA	GCAGGAAGGG	TTGATGATGG	GCTGGAGCTT	
		1,749	1,759	1,769	1,779	1,789	1,799	1,809
seqidno16	CGTAGTGACC	TTTACTACAC	TCATTAATGG	CTACTGTAAG	GCAGGAAGGG	TTGATGATGG	GCTGGAGCTT	
Similarity								
		1,830	1,840	1,850	1,860	1,870	1,880	1,890
		1,819	1,829	1,839	1,849	1,859	1,869	1,879
seqidno2	TTCTGCGAGA	TGGGTCGAAG	AGGGATAGTT	GCTAACGCAA	TTACTTACAT	CACTTTGATT	TGTGGTTTTC	
		1,825	1,835	1,845	1,855	1,865	1,875	1,885
seqidno18	TTCTGCGAGA	TGGGTAGAAG	AGGGATAGTT	GCTAATACAA	TTACTTACAT	CACTTTGATT	CGTGGTTTTC	
		1,819	1,829	1,839	1,849	1,859	1,869	1,879
seqidno16	TTCTGCGAGA	TGGGTCGAAG	AGGGATAGTT	GCTAACGCAA	TTACTTACAT	CACTTTGATT	TGTGGTTTTC	
Similarity								
		1,900	1,910	1,920	1,930	1,940	1,950	1,960
		1,889	1,899	1,909	1,919	1,929	1,939	1,949
seqidno2	GTAAAGTGGG	TAATATTAAT	GGGGCTCTAG	ACATTTTCCA	GGAGATGATT	TCAAGTGGTG	TGTATCCTGA	
		1,895	1,905	1,915	1,925	1,935	1,945	1,955
seqidno18	GCAATGTGGG	TAATATTAAT	GGGGCTCTAG	ACATTTTCCA	GGAGATGATT	TCAAGTGGTG	TGTATCCTGG	
		1,889	1,899	1,909	1,919	1,929	1,939	1,949
seqidno16	GTAAAGTGGG	TAATATTAAT	GGGGCTCTAG	ACATTTTCCA	GGAGATGATT	TCAAGTGGTG	TGTATCCTGA	
Similarity								
		1,970	1,980	1,990	2,000	2,010	2,020	2,030
		1,959	1,969	1,979	1,989	1,999	2,009	2,019
seqidno2	TACCATTACC	ATCCGCAATA	TGCTGACTGG	TTTATGGAGT	AAAGAGGAAC	TAAAAGGGC	AGTGGCAATG	
		1,965	1,975	1,985	1,995	2,005	2,015	2,025
seqidno18	TATCATTACT	ATCCGCAATA	TGCTGACTGG	TTTATGGAGT	AAAGAGGAAC	TAAAAGGAC	AGTGGCAATG	
		1,959	1,969	1,979	1,989	1,999	2,009	2,019
seqidno16	TACCATTACC	ATCCGCAATA	TGCTGACTGG	TTTATGGAGT	AAAGAGGAAC	TAAAAGGGC	AGTGGCAATG	
Similarity								
		2,040	2,050	2,060	2,070	2,079		
		2,029	2,039	2,049	2,064			
seqidno2	CTTGAGAAAC	TGCAGATGAG	TATGGATCTA	TCATTGGGG	GATGA----			
		2,035	2,045	2,054	2,064	2,073		
seqidno18	CTTGAGGAAC	TGCAGATGAG	TGTGGGG-TA	TCAGTTGGAG	GATGAATGA			
		2,029	2,039	2,049	2,064			
seqidno16	CTTGAGAAAC	TGCAGATGAG	TATGGATCTA	TCATTGGGG	GATGA----			
Similarity								